

Figure 1

1	GGCACGAGGTGCACAGGAAGGATGAGGAAGACCAGGCTCTGGGGCTGCTGTGGATGCTC	60
1	M R K T R L W G L L W M L	13
61	TTTGTCTCAGAACTCCGAGCTGCAACTAAATTAACGTAGGAAAAGTATGAACTGAAAGAG	120
14	F V S E L R A A T K L T E E K Y E L K E	33
121	GGGCAGACCCCTGGATGTGAAATGTGACTACACGCTAGAGAAGTTGCCAGCAGCCAGAAA	180
34	G Q T L D V K C D Y T L E K F A S S Q K	53
181	GCTTGGCAGATAATAAGGGACGGAGAGATGCCAAGACCCCTGGCATGCACAGAGAGGCCT	240
54	A W Q I I R D G E M P K T L A C T E R P	73
241	TCAAAGAATTCCCATCCAGTCCAAGTGGGAGGATCATACTAGAAGACTACCATGATCAT	300
74	S K N S H P V Q V G R I I L E D Y H D H	93
301	GGTTTACTGCGCGTCCGAATGGTCAACCTCAAGTGGAAAGATTCTGGACTGTATCAGTGT	360
94	G L L R V R M V N L Q V E D S G L Y Q C	113
361	GTGATCTACCAGCCTCCCAAGGAGCCTCACATGCTGTTGATCGATCCGTTGGTGGTG	420
114	V I Y Q P P K E P H M L F D R I R L V V	133
421	ACCAAGGGTTTCAGGGACCCCTGGCTCCAATGAGAATTCTACCCAGAATGTGTATAAG	480
134	T K G F S G T P G S N E N S T Q N V Y K	153
481	ATTCCTCCTACCACCACTAAGGCCTTGTGCCACTCTATACCAGCCCCAGAACGTGACC	540
154	I P P T T T K A L C P L Y T S P R T V T	173
541	CAAGCTCCACCCAAGTCACGTGCCATGCTCCACTCCTGACTCTGAAATCAACCTTACA	600
174	Q A P P K S T A D V S T P D S E I N L T	193
601	AATGTGACAGATATCATCAGGGTCCGGTGTCAACATTGTCAATTCTGGCTGGTGGA	660
194	N V T D I I R V P V F N I V I L L A G G	213
661	TTCCTGAGTAAGAGCCTGGCTTCTCTGTCCCTGTTGCTGTCACGCTGAGGTCAATTGTA	720
214	F L S K S L V F S V L F A V T L R S F V	233
721	CCCTAGGCCACGAACCCACGAGAATGTCCTCTGACTTCCAGCCACATCCATCTGGCACT	780
234	P *	235
781	TGTGCCAAGGGAGGAGGGAGGAGGTAAAGGCAGGGAGTTAATAACATGAATTAAATCTG	840
841	TAATCACCAAGCTAAAAAAAAAAAAAA	870

Figure 2

